

SEQUENCE LISTING

<110> Allain, Eric
Wenger, Kevin S
Bisgård-Frantzen, Henrik

<120> Process for producing a fermentation product

<130> 10674.204-WO

<160> 41

<170> PatentIn version 3.3

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-15

-10

-5

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gtt gcc aag aat ggc gta ctt tgc aac att ggt agc cag gga tgc atg Val Ala Lys Asn Gly Val Leu Cys Asn Ile Gly Ser Gln Gly Cys Met 15 20 25 30	144
tct gag ggt gcc tat agc ggt att gtg atc gca tct ccc tct aaa act Ser Glu Gly Ala Tyr Ser Gly Ile Val Ile Ala Ser Pro Ser Lys Thr 35 40 45	192
agc cct gac tat ctc t gtgagtatta ttgtgtaaagt agcctcactg atagtacatt Ser Pro Asp Tyr Leu 50	248
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gat acg gtatgtggca tcnegcttcc ggctcgctc aaagatgnaa aattgatgtt Asp Thr 75	404
tcttag aca ctg cgc act ctc att gac gag ttt gtc tct gcg gaa gcc Thr Leu Arg Thr Leu Ile Asp Glu Phe Val Ser Ala Glu Ala 80 85	452
acc att caa caa acc agt aac cca tct ggt acc gtc tct acc ggt ggt Thr Ile Gln Gln Thr Ser Asn Pro Ser Gly Thr Val Ser Thr Gly Gly 90 95 100 105	500
ctc ggc gaa ccc aaa ttc aat atc gac gag acg gca ttt acg ggc gca Leu Gly Glu Pro Lys Phe Asn Ile Asp Glu Thr Ala Phe Thr Gly Ala 110 115 120	548
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tactatctat aatttctag ccc caa cgt gat ggt ccc gcc ctc cgt gca acc Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr 125 130 135	649
gca atc atg acc tat gcg acg tat ctg tac aac aat ggc aac act tcc Ala Ile Met Thr Tyr Ala Thr Tyr Leu Tyr Asn Asn Gly Asn Thr Ser 140 145 150	697
tac gtg acc aac acc ctt tgg cct atc atc aag ctc gac ctt gac tat Tyr Val Thr Asn Thr Leu Trp Pro Ile Ile Lys Leu Asp Leu Asp Tyr 155 160 165	745
gtc aac tcg gac tgg aac cag acc a gtaagcgaat ttctaggggg Val Asn Ser Asp Trp Asn Gln Thr 170 175	790

acttatctaa aacagcatat tcaaccagta aatag cg ttt gac ctc tgg gaa	842
Thr Phe Asp Leu Trp Glu	180
gaa gtt gac tcg tct tct ttc ttt acg act gcc gtt cag cac cgt gct	890
Glu Val Asp Ser Ser Ser Phe Phe Thr Thr Ala Val Gln His Arg Ala	185 190 195
ctt gtt cag ggc gca gcc ttt gct acc ctc atc ggc caa act tcg tct	938
Leu Val Gln Gly Ala Ala Phe Ala Thr Leu Ile Gly Gln Thr Ser Ser	200 205 210
gct tcg act tac tcc gcc acg gcc cct agc att ctc tgc ttc ttg cag	986
Ala Ser Thr Tyr Ser Ala Thr Ala Pro Ser Ile Leu Cys Phe Leu Gln	215 220 225
gtgagataaa aatcttttcta tgtaattgggt ttttcccctc aaattgaaat tgacatattt	1046
gcgatccaat ag tct tac tgg aac acc aac gga tac tgg acg gcc aac act	1097
Ser Tyr Trp Asn Thr Asn Gly Tyr Trp Thr Ala Asn Thr	230 235 240
ggg ggc gga cgt tcc ggc aag gac gcc aac acc ata ctc gct tct atc	1145
Gly Gly Gly Arg Ser Gly Lys Asp Ala Asn Thr Ile Leu Ala Ser Ile	245 250 255
cac aca ttt gac gcc agc gcc ggc tgc tct gct gcc acg tct caa cca	1193
His Thr Phe Asp Ala Ser Ala Gly Cys Ser Ala Ala Thr Ser Gln Pro	260 265 270
tgc tct gac gta gca ttg gcc aac ctg aag gta tac gtt gac tct ttc	1241
Cys Ser Asp Val Ala Leu Ala Asn Leu Lys Val Tyr Val Asp Ser Phe	275 280 285 290
cgt agt att tat acg atc aac agc ggt att tcc tct acc tcg ggt gtt	1289
Arg Ser Ile Tyr Thr Ile Asn Ser Gly Ile Ser Ser Thr Ser Gly Val	295 300 305
gct act ggt cgc tac ccc gaa gat tcg tat tac aat ggc aac	1331
Ala Thr Gly Arg Tyr Pro Glu Asp Ser Tyr Tyr Asn Gly Asn	310 315 320
gtacgtattt atctaatttt tocaagacag tcaaagttaa tgttcattctg ccccttttta	1391
cctgtacatt caaaatag ccc tgg tac ctc tgc aca ctc gcc gtc gcc gag	1442
Pro Trp Tyr Leu Cys Thr Leu Ala Val Ala Glu	325 330
cag ctc tat gat gct ctc atc gta tgg aag gct gcc ggg gag ctc aac	1490
Gln Leu Tyr Asp Ala Leu Ile Val Trp Lys Ala Ala Gly Glu Leu Asn	335 340 345
gtc acc tcc gtc tcg ctc gcg ttc ttc cag caa ttc gac tcg agc atc	1538
Val Thr Ser Val Ser Leu Ala Phe Phe Gln Gln Phe Asp Ser Ser Ile	350 355 360
acc gcc ggc act tac gcc tcc tcg tcg agc gta tac act tcg ctc atc	1586
Thr Ala Gly Thr Tyr Ala Ser Ser Ser Ser Val Tyr Thr Ser Leu Ile	365 370 375

tct gac atc cag gcg ttc gca gac gag ttt gtt gac att gtt gcc aag 1634
 Ser Asp Ile Gln Ala Phe Ala Asp Glu Phe Val Asp Ile Val Ala Lys
 380 385 390 395

tac acg cct tcg tct ggc ttc ttg tct gag cag tat gat aag tcc acg 1682
 Tyr Thr Pro Ser Ser Gly Phe Leu Ser Glu Gln Tyr Asp Lys Ser Thr
 400 405 410

ggt gct cag gat tcg gct gct aac ttg act t gtaagtcac tattgttca 1733
 Gly Ala Gln Asp Ser Ala Ala Asn Leu Thr
 415 420

ttctattcct tttcaaaaaa aaaagtgatg ctaatgattt ttggcggaaa ccag gg 1789
 Trp

tcc tat gct gct gct atc acc gct tac caa gcc cgc aat ggc ttc aca 1837
 Ser Tyr Ala Ala Ala Ile Thr Ala Tyr Gln Ala Arg Asn Gly Phe Thr
 425 430 435

ggt gct tcg tgg ggt gct aag gga gtt tct acc tcc tgc tcg act ggt 1885
 Gly Ala Ser Trp Gly Ala Lys Gly Val Ser Thr Ser Cys Ser Thr Gly
 440 445 450

gct aca agc ccg ggt ggc tcc tcg ggt agt gtc gag gtc act ttc gac 1933
 Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe Asp
 455 460 465 470

gtt tac gct acc aca gta tat ggc c gtaagcactt gactagcttc 1978
 Val Tyr Ala Thr Thr Val Tyr Gly
 475

aaaccatact tcatcatgct gataaaca aaatgaaac ag ag aac atc tat 2031
 Gln Asn Ile Tyr
 480

atc acc ggt gat gtg agt gag ctc ggc aac tgg aca ccc gcc aat ggt 2079
 Ile Thr Gly Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly
 485 490 495

gtt gca ctc tct tct gct aac tac ccc acc tgg agt g gtaagttgac 2126
 Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser
 500 505 510

ccttaccagt atcttgacag acattgatat tgacttccgc aatacag cc acg atc 2181
 Ala Thr Ile

gct ctc ccc gct gac acg aca atc cag tac aag tat gtc aac att gac 2229
 Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp
 515 520 525

ggc agc acc gtc atc tgg gag gat gct atc agc aat cgc gag atc acg 2277
 Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr
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<211> 579
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<213> Athelia rolfsii
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.<400> 2

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-1 1 5 10

Val Ala Lys Asn Gly Val Leu Cys Asn Ile Gly Ser Gln Gly Cys Met
15 20 25 30

Ser Glu Gly Ala Tyr Ser Gly Ile Val Ile Ala Ser Pro Ser Lys Thr
35 40 45

Ser Pro Asp Tyr Leu Tyr Thr Trp Thr Arg Asp Ser Ser Leu Val Phe
50 55 60

Lys Met Leu Ile Asp Gln Tyr Thr Asn Gly Leu Asp Thr Thr Leu Arg
65 70 75

Thr Leu Ile Asp Glu Phe Val Ser Ala Glu Ala Thr Ile Gln Gln Thr
80 85 90

Ser Asn Pro Ser Gly Thr Val Ser Thr Gly Gly Leu Gly Glu Pro Lys
95 100 105 110

Phe Asn Ile Asp Glu Thr Ala Phe Thr Gly Ala Trp Gly Arg Pro Gln
115 120 125

Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Ile Met Thr Tyr Ala Thr
130 135 140

Tyr Leu Tyr Asn Asn Gly Asn Thr Ser Tyr Val Thr Asn Thr Leu Trp
145 150 155

Pro Ile Ile Lys Leu Asp Leu Asp Tyr Val Asn Ser Asp Trp Asn Gln
 160 165 170

Thr Thr Phe Asp Leu Trp Glu Glu Val Asp Ser Ser Ser Phe Phe Thr
 175 180 185 190

Thr Ala Val Gln His Arg Ala Leu Val Gln Gly Ala Ala Phe Ala Thr
 195 200 205

Leu Ile Gly Gln Thr Ser Ser Ala Ser Thr Tyr Ser Ala Thr Ala Pro
 210 215 220

Ser Ile Leu Cys Phe Leu Gln Ser Tyr Trp Asn Thr Asn Gly Tyr Trp
 225 230 235

Thr Ala Asn Thr Gly Gly Gly Arg Ser Gly Lys Asp Ala Asn Thr Ile
 240 245 250

Leu Ala Ser Ile His Thr Phe Asp Ala Ser Ala Gly Cys Ser Ala Ala
 255 260 265 270

Thr Ser Gln Pro Cys Ser Asp Val Ala Leu Ala Asn Leu Lys Val Tyr
 275 280 285

Val Asp Ser Phe Arg Ser Ile Tyr Thr Ile Asn Ser Gly Ile Ser Ser
 290 295 300

Thr Ser Gly Val Ala Thr Gly Arg Tyr Pro Glu Asp Ser Tyr Tyr Asn
 305 310 315

Gly Asn Pro Trp Tyr Leu Cys Thr Leu Ala Val Ala Glu Gln Leu Tyr
 320 325 330

Asp Ala Leu Ile Val Trp Lys Ala Ala Gly Glu Leu Asn Val Thr Ser
 335 340 345 350

Val Ser Leu Ala Phe Phe Gln Gln Phe Asp Ser Ser Ile Thr Ala Gly
 355 360 365

Thr Tyr Ala Ser Ser Ser Ser Val Tyr Thr Ser Leu Ile Ser Asp Ile
 370 375 380

Gln Ala Phe Ala Asp Glu Phe Val Asp Ile Val Ala Lys Tyr Thr Pro
 385 390 395

Ser Ser Gly Phe Leu Ser Glu Gln Tyr Asp Lys Ser Thr Gly Ala Gln
400 405 410

Asp Ser Ala Ala Asn Leu Thr Trp Ser Tyr Ala Ala Ala Ile Thr Ala
415 420 425 430

Tyr Gln Ala Arg Asn Gly Phe Thr Gly Ala Ser Trp Gly Ala Lys Gly
435 440 445

Val Ser Thr Ser Cys Ser Thr Gly Ala Thr Ser Pro Gly Gly Ser Ser
450 455 460

Gly Ser Val Glu Val Thr Phe Asp Val Tyr Ala Thr Thr Val Tyr Gly
465 470 475

Gln Asn Ile Tyr Ile Thr Gly Asp Val Ser Glu Leu Gly Asn Trp Thr
480 485 490

Pro Ala Asn Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser
495 500 505 510

Ala Thr Ile Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val
515 520 525

Asn Ile Asp Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg
530 535 540

Glu Ile Thr Thr Pro Ala Ser Gly Thr Tyr Thr Glu Lys Asp Thr Trp
545 550 555

Asp Glu Ser
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<213> Aspergillus niger

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Gly Asn Glu Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asp His
 35 40 45

Leu Asp Tyr Ile Glu Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
 50 55 60

Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
 65 70 75 80

Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
 85 90 95

Ala Asp Asn Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
 100 105 110

Tyr Leu Met Val Asp Val Val Pro Asp His Met Gly Tyr Ala Gly Asn
 115 120 125

Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
 130 135 140

Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
 145 150 155 160

Val Glu Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
 165 170 175

Asp Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala
 180 185 190

Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
 195 200 205

Leu Glu Val Gln Pro Asp Phe Phe Pro Gly Tyr Asn Lys Ala Ser Gly
 210 215 220

Val Tyr Cys Val Gly Glu Ile Asp Asn Gly Asn Pro Ala Ser Asp Cys
 225 230 235 240

Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
 245 250 255

Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu
 260 265 270

Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
 275 280 285

Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Lys Tyr
 290 295 300

Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu
 305 310 315 320

Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ala
 325 330 335

Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
 340 345 350

Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile
 355 360 365

Arg Lys Leu Ala Ile Ala Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn
 370 375 380

Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Ala Lys Gly Thr
 385 390 395 400

Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
 405 410 415

Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
 420 425 430

Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
 435 440 445

Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu
 450 455 460

Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg
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Leu Tyr Val Glu

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 <211> 498
 <212> PRT
 <213> *Aspergillus oryzae*

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Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
 15 20 25

Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
 30 35 40 45

Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
 50 55 60

Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
 65 70 75

Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
 80 85 90

Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
 95 100 105

Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
 110 115 120 125

Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
 130 135 140

Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
 145 150 155

Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
 160 165 170

Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
 175 180 185

Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
 190 195 200 205

Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
 210 215 220

Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
 225 230 235

Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
 240 245 250

Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
 255 260 265

Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
 270 275 280 285

Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
 290 295 300

Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
 305 310 315

Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
 320 325 330

Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
 335 340 345

Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
 350 355 360 365

Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
 370 375 380

Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
 385 390 395

Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
 400 405 410

Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
 415 420 425

Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
 430 435 440 445

Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
 450 455 460

Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
 465 470 475

Ser Ser

<210> 5
 <211> 483
 <212> PRT
 <213> Bacillus licheniformis

<220>
 <221> mat_peptide
 <222> (1)..(483)

<400> 5

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Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45

Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
 50 55 60

Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 75 80

Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
 85 90 95

Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
 100 105 110

Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
 115 120 125

Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
 130 135 140

Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
 145 150 155 160

Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
 165 170 175

Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
 180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
 195 200 205

Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
 210 215 220

Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
 225 230 235 240

Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
 245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
 260 265 270

Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
 275 280 285

His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
 290 295 300

Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
 305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
355 360 365

Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385 390 395 400

Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
405 410 415

Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
435 440 445

Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
450 455 460

Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465 470 475 480

Val Gln Arg

<210> 6
<211> 480
<212> PRT
<213> Bacillus amyloliquefaciens

<220>
<221> mat_peptide
<222> (1)..(480)

<400> 6

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Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
20 25 30

Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
35 40 45

Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
50 55 60

Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
65 70 75 80

Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
85 90 95

Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
100 105 110

Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
115 120 125

Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
130 135 140

Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145 150 155 160

Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
165 170 175

Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
195 200 205

Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
210 215 220

Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225 230 235 240

Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
260 265 270

Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
 275 280 285

His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Tyr Asp Met
 290 295 300

Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
 305 310 315 320

Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
 340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365

Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
 370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
 385 390 395 400

Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
 405 410 415

Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430

Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
 435 440 445

Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
 450 455 460

Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
 465 470 475 480

<210> 7

<211> 514

<212> PRT

<213> Bacillus stearothermophilus

<220>

<221> mat_peptide

<222> (1)..(514)

<400> 7

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Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn
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Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys
 35 40 45

Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp
 50 55 60

Leu Gly Glu Phe Asn Gln Lys Gly Ala Val Arg Thr Lys Tyr Gly Thr
 65 70 75 80

Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met
 85 90 95

Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly
 100 105 110

Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln
 115 120 125

Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe
 130 135 140

Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His
 145 150 155 160

Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr
 165 170 175

Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu
 180 185 190

Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His
 195 200 205

Pro Glu Val Val Thr Glu Leu Lys Ser Trp Gly Lys Trp Tyr Val Asn
 210 215 220

Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys
225 230 235 240

Phe Ser Phe Phe Pro Asp Trp Leu Ser Asp Val Arg Ser Gln Thr Gly
245 250 255

Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys
260 265 270

Leu His Asn Tyr Ile Met Lys Thr Asn Gly Thr Met Ser Leu Phe Asp
275 280 285

Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Thr
290 295 300

Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro
305 310 315 320

Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln
325 330 335

Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala
340 345 350

Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp
355 360 365

Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile
370 375 380

Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
385 390 395 400

Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Val
405 410 415

Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val
435 440 445

Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
450 455 460

Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
 465 470 475 480

Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Trp Ser Ile Thr Thr
 485 490 495

Arg Pro Trp Thr Asp Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
 500 505 510

Ala Trp

<210> 8
 <211> 38
 <212> PRT
 <213> Aspergillus niger

<220>
 <221> MISC_FEATURE
 <222> (1)..(38)
 <223> linker sequence

<400> 8

Thr Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val
 1 5 10 15

Thr Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser
 20 25 30

Thr Ser Ser Thr Ser Ala
 35

<210> 9
 <211> 31
 <212> PRT
 <213> Aspergillus kawachi

<220>
 <221> MISC_FEATURE
 <222> (1)..(31)
 <223> linker sequence

<400> 9

Thr Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr
 1 5 10 15

Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser
 20 25 30

<210> 10
 <211> 11
 <212> PRT
 <213> Athelia rolfsii

<220>
 <221> MISC_FEATURE
 <222> (1)..(11)
 <223> linker sequence

<400> 10

Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser
 1 5 10

<210> 11
 <211> 8
 <212> PRT
 <213> Artificial

<220>
 <223> PEPT linker

<220>
 <221> MISC_FEATURE
 <222> (1)..(8)
 <223> linker sequence

<400> 11

Pro Glu Pro Thr Pro Glu Pro Thr
 1 5

<210> 12
 <211> 396
 <212> DNA
 <213> Aspergillus kawachi

<220>
 <221> CDS
 <222> (1)..(396)
 <223> CBM

<400> 12
 act agt aca tcc aaa gcc acc acc tcc tct tct tct tct tct gct gct
 Thr Ser Thr Ser Lys Ala Thr Thr Ser Ser Ser Ser Ser Ser Ala Ala
 1 5 10 15

48

gct act act tct tca tca tgc acc gca aca agc acc acc ctc ccc atc
 Ala Thr Thr Ser Ser Cys Thr Ala Thr Ser Thr Thr Leu Pro Ile
 20 25 30

96

acc ttc gaa gaa ctc gtc acc act acc tac ggg gaa gaa gtc tac ctc 144
 Thr Phe Glu Glu Leu Val Thr Thr Thr Tyr Gly Glu Glu Val Tyr Leu
 35 40 45

agc gga tct atc tcc cag ctc gga gag tgg gat acg agt gac gcg gtg 192
 Ser Gly Ser Ile Ser Gln Leu Gly Glu Trp Asp Thr Ser Asp Ala Val
 50 55 60

aag ttg tcc gcg gat gat tat acc tcg agt aac ccc gag tgg tct gtt 240
 Lys Leu Ser Ala Asp Asp Tyr Thr Ser Ser Asn Pro Glu Trp Ser Val
 65 70 75 80

act gtg tcg ttg ccg gtg ggg acg acc ttc gag tat aag ttt att aag 288
 Thr Val Ser Leu Pro Val Gly Thr Thr Phe Glu Tyr Lys Phe Ile Lys
 85 90 95

gtc gat gag ggt gga agt gtg act tgg gaa agt gat ccg aat agg gag 336
 Val Asp Glu Gly Gly Ser Val Thr Trp Glu Ser Asp Pro Asn Arg Glu
 100 105 110

tat act gtg cct gaa tgt ggg aat ggg agt ggg gag acg gtg gtt gat 384
 Tyr Thr Val Pro Glu Cys Gly Asn Gly Ser Gly Glu Thr Val Val Asp
 115 120 125

acg tgg agg tag 396
 Thr Trp Arg
 130

<210> 13
 <211> 131
 <212> PRT
 <213> Aspergillus kawachi

<400> 13

Thr Ser Thr Ser Lys Ala Thr Thr Ser Ser Ser Ser Ser Ser Ala Ala
 1 5 10 15

Ala Thr Thr Ser Ser Ser Cys Thr Ala Thr Ser Thr Thr Leu Pro Ile
 20 25 30

Thr Phe Glu Glu Leu Val Thr Thr Thr Tyr Gly Glu Glu Val Tyr Leu
 35 40 45

Ser Gly Ser Ile Ser Gln Leu Gly Glu Trp Asp Thr Ser Asp Ala Val
 50 55 60

Lys Leu Ser Ala Asp Asp Tyr Thr Ser Ser Asn Pro Glu Trp Ser Val
 65 70 75 80

Thr Val Ser Leu Pro Val Gly Thr Thr Phe Glu Tyr Lys Phe Ile Lys
 85 90 95

Val Asp Glu Gly Gly Ser Val Thr Trp Glu Ser Asp Pro Asn Arg Glu
 100 105 110

Tyr Thr Val Pro Glu Cys Gly Asn Gly Ser Gly Glu Thr Val Val Asp
 115 120 125

Thr Trp Arg
 130

<210> 14
 <211> 102
 <212> PRT
 <213> Bacillus flavothermus

<220>
 <221> MISC_FEATURE
 <222> (1)..(102)
 <223> CBM

<400> 14

Ile Ser Thr Thr Ser Gln Ile Thr Phe Thr Val Asn Asn Ala Thr Thr
 1 5 10 15

Val Trp Gly Gln Asn Val Tyr Val Val Gly Asn Ile Ser Gln Leu Gly
 20 25 30

Asn Trp Asp Pro Val His Ala Val Gln Met Thr Pro Ser Ser Tyr Pro
 35 40 45

Thr Trp Thr Val Thr Ile Pro Leu Leu Gln Gly Gln Asn Ile Gln Phe
 50 55 60

Lys Phe Ile Lys Lys Asp Ser Ala Gly Asn Val Ile Trp Glu Asp Ile
 65 70 75 80

Ser Asn Arg Thr Tyr Thr Val Pro Thr Ala Ala Ser Gly Ala Tyr Thr
 85 90 95

Ala Ser Trp Asn Val Pro
 100

<210> 15
 <211> 99
 <212> PRT
 <213> Bacillus sp.

<220>

<221> MISC_FEATURE

<222> (1)..(99)

<223> CBM

<400> 15

Thr Ser Asn Val Thr Phe Thr Val Asn Asn Ala Thr Thr Val Tyr Gly
 1 5 10 15

Gln Asn Val Tyr Val Val Gly Asn Ile Pro Glu Leu Gly Asn Trp Asn
 20 25 30

Ile Ala Asn Ala Ile Gln Met Thr Pro Ser Ser Tyr Pro Thr Trp Lys
 35 40 45

Thr Thr Val Ser Leu Pro Gln Gly Lys Ala Ile Glu Phe Lys Phe Ile
 50 55 60

Lys Lys Asp Ser Ala Gly Asn Val Ile Trp Glu Asn Ile Ala Asn Arg
 65 70 75 80

Thr Tyr Thr Val Pro Phe Ser Ser Thr Gly Ser Tyr Thr Ala Asn Trp
 85 90 95

Asn Val Pro

<210> 16

<211> 102

<212> PRT

<213> Alcaliphilic Bacillus

<220>

<221> MISC_FEATURE

<222> (1)..(102)

<223> CBM

<400> 16

Thr Ser Thr Thr Ser Gln Ile Thr Phe Thr Val Asn Asn Ala Thr Thr
 1 5 10 15

Val Trp Gly Gln Asn Val Tyr Val Val Gly Asn Ile Ser Gln Leu Gly
 20 25 30

Asn Trp Asp Pro Val Asn Ala Val Gln Met Thr Pro Ser Ser Tyr Pro
 35 40 45

Thr Trp Val Val Thr Val Pro Leu Pro Gln Ser Gln Asn Ile Gln Phe
50 55 60

Lys Phe Ile Lys Lys Asp Gly Ser Gly Asn Val Ile Trp Glu Asn Ile
65 70 75 80

Ser Asn Arg Thr Tyr Thr Val Pro Thr Ala Ala Ser Gly Ala Tyr Thr
85 90 95

Ala Asn Trp Asn Val Pro
100

<210> 17
<211> 112
<212> PRT
<213> Hormoconis resinae

<220>
<221> MISC_FEATURE
<222> (1)..(112)
<223> CBM

<400> 17

Cys Gln Val Ser Ile Thr Phe Asn Ile Asn Ala Thr Thr Tyr Tyr Gly
1 5 10 15

Glu Asn Leu Tyr Val Ile Gly Asn Ser Ser Asp Leu Gly Ala Trp Asn
20 25 30

Ile Ala Asp Ala Tyr Pro Leu Ser Ala Ser Ala Tyr Thr Gln Asp Arg
35 40 45

Pro Leu Trp Ser Ala Ala Ile Pro Leu Asn Ala Gly Glu Val Ile Ser
50 55 60

Tyr Gln Tyr Val Arg Gln Glu Asp Cys Asp Gln Pro Tyr Ile Tyr Glu
65 70 75 80

Thr Val Asn Arg Thr Leu Thr Val Pro Ala Cys Gly Gly Ala Ala Val
85 90 95

Thr Thr Asp Asp Ala Trp Met Gly Pro Val Gly Ser Ser Gly Asn Cys
100 105 110

<210> 18
<211> 95
<212> PRT

<213> Lentinula edodes

<220>

<221> MISC_FEATURE

<222> (1)..(95)

<223> CBM

<400> 18

Val Ser Val Thr Phe Asn Val Asp Ala Ser Thr Leu Glu Gly Gln Asn
1 5 10 15

Val Tyr Leu Thr Gly Ala Val Asp Ala Leu Glu Asp Trp Ser Thr Asp
20 25 30

Asn Ala Ile Leu Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Val Thr
35 40 45

Val Asp Leu Pro Gly Ser Thr Asp Val Gln Tyr Lys Tyr Ile Lys Lys
50 55 60

Asp Gly Ser Gly Thr Val Thr Trp Glu Ser Asp Pro Asn Met Glu Ile
65 70 75 80

Thr Thr Pro Ala Asn Gly Thr Tyr Ala Thr Asn Asp Thr Trp Arg
85 90 95

<210> 19

<211> 107

<212> PRT

<213> Neurospora crassa

<220>

<221> MISC_FEATURE

<222> (1)..(107)

<223> CBM

<400> 19

Cys Ala Ala Asp His Glu Val Leu Val Thr Phe Asn Glu Lys Val Thr
1 5 10 15

Thr Ser Tyr Gly Gln Thr Val Lys Val Val Gly Ser Ile Ala Ala Leu
20 25 30

Gly Asn Trp Ala Pro Ala Ser Gly Val Thr Leu Ser Ala Lys Gln Tyr
35 40 45

Ser Ser Ser Asn Pro Leu Trp Ser Thr Thr Ile Ala Leu Pro Gln Gly
 50 55 60

Thr Ser Phe Lys Tyr Lys Tyr Val Val Val Asn Ser Asp Gly Ser Val
 65 70 75 80

Lys Trp Glu Asn Asp Pro Asp Arg Ser Tyr Ala Val Gly Thr Asp Cys
 85 90 95

Ala Ser Thr Ala Thr Leu Asp Asp Thr Trp Arg
 100 105

<210> 20
 <211> 115
 <212> PRT
 <213> Talaromyces byssochlamydioides

<220>
 <221> MISC_FEATURE
 <222> (1)..(115)
 <223> CBM

<400> 20

Thr Thr Thr Gly Ala Ala Pro Cys Thr Thr Pro Thr Thr Val Ala Val
 1 5 10 15

Thr Phe Asp Glu Ile Val Thr Thr Thr Tyr Gly Glu Thr Val Tyr Leu
 20 25 30

Ser Gly Ser Ile Pro Ala Leu Gly Asn Trp Asp Thr Ser Ser Ala Ile
 35 40 45

Ala Leu Ser Ala Val Asp Tyr Thr Ser Ser Asn Pro Leu Trp Tyr Val
 50 55 60

Thr Val Asn Leu Pro Ala Gly Thr Ser Phe Glu Tyr Lys Phe Phe Val
 65 70 75 80

Gln Gln Thr Asp Gly Thr Ile Val Trp Glu Asp Asp Pro Asn Arg Ser
 85 90 95

Tyr Thr Val Pro Ala Asn Cys Gly Gln Thr Thr Ala Ile Ile Asp Asp
 100 105 110

Ser Trp Gln
 115

<210> 21
 <211> 115
 <212> PRT
 <213> Geosmithia cylindrospora

<220>
 <221> MISC_FEATURE
 <222> (1)..(115)
 <223> CBM

<400> 21

Thr Ser Thr Gly Ser Ala Pro Cys Thr Thr Pro Thr Thr Val Ala Val
 1 5 10 15

Thr Phe Asp Glu Ile Val Thr Thr Ser Tyr Gly Glu Thr Val Tyr Leu
 20 25 30

Ala Gly Ser Ile Ala Ala Leu Gly Asn Trp Asp Thr Asn Ser Ala Ile
 35 40 45

Ala Leu Ser Ala Ala Asp Tyr Thr Ser Asn Asn Asn Leu Trp Tyr Val
 50 55 60

Thr Val Asn Leu Ala Ala Gly Thr Ser Phe Gln Tyr Lys Phe Phe Val
 65 70 75 80

Lys Glu Thr Asp Ser Thr Ile Val Trp Glu Asp Asp Pro Asn Arg Ser
 85 90 95

Tyr Thr Val Pro Ala Asn Cys Gly Gln Thr Thr Ala Ile Ile Asp Asp
 100 105 110

Thr Trp Gln
 115

<210> 22
 <211> 139
 <212> PRT
 <213> Scorias spongiosa CBM

<220>
 <221> MISC_FEATURE
 <222> (1)..(139)
 <223> CBM

<400> 22

Ala Lys Val Pro Ser Thr Cys Ser Ala Ser Ser Ala Thr Gly Thr Cys
1 5 10 15

Thr Thr Ala Thr Ser Thr Phe Gly Gly Ser Thr Pro Thr Thr Ser Cys
20 25 30

Ala Thr Thr Pro Thr Leu Thr Thr Val Leu Phe Asn Glu Arg Ala Thr
35 40 45

Thr Asn Phe Gly Gln Asn Val His Leu Thr Gly Ser Ile Ser Gln Leu
50 55 60

Gly Ser Trp Asp Thr Asp Ser Ala Val Ala Leu Ser Ala Val Asn Tyr
65 70 75 80

Thr Ser Ser Asp Pro Leu Trp Phe Val Arg Val Gln Leu Pro Ala Gly
85 90 95

Thr Ser Phe Gln Tyr Lys Tyr Phe Lys Lys Asp Ser Ser Asn Ala Val
100 105 110

Ala Trp Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Leu Asn Cys
115 120 125

Ala Gly Thr Ala Thr Glu Asn Asp Thr Trp Arg
130 135

<210> 23
<211> 126
<212> PRT
<213> Eupenicillium ludwigii

<220>
<221> MISC_FEATURE
<222> (1)..(126)
<223> CBM

<400> 23

Ser Thr Thr Thr Thr Ser Thr Thr Lys Thr Thr Thr Thr Ser Thr Thr
1 5 10 15

Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Ile
20 25 30

Ala Thr Thr Tyr Tyr Gly Glu Asn Ile Lys Ile Ala Gly Ser Ile Ser
35 40 45

Gln Leu Gly Asp Trp Asp Thr Ser Asn Ala Val Ala Leu Ser Ala Ala
 50 55 60

Asp Tyr Thr Ser Ser Asp His Leu Trp Phe Val Asp Ile Asp Leu Pro
 65 70 75 80

Ala Gly Thr Val Phe Glu Tyr Lys Tyr Ile Arg Ile Glu Ser Asp Gly
 85 90 95

Ser Ile Glu Trp Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Ala
 100 105 110

Ala Cys Ala Thr Thr Ala Val Thr Glu Asn Asp Thr Trp Arg
 115 120 125

<210> 24
 <211> 116
 <212> PRT
 <213> Aspergillus japonicus

<220>
 <221> MISC_FEATURE
 <222> (1)..(116)
 <223> CBM

<400> 24

Lys Thr Ser Thr Thr Thr Ser Ser Cys Ser Thr Pro Thr Ser Val Ala
 1 5 10 15

Val Thr Phe Asp Val Ile Ala Thr Thr Thr Tyr Gly Glu Asn Val Tyr
 20 25 30

Ile Ser Gly Ser Ile Ser Gln Leu Gly Ser Trp Asp Thr Ser Ser Ala
 35 40 45

Ile Ala Leu Ser Ala Ser Gln Tyr Thr Ser Ser Asn Asn Leu Trp Tyr
 50 55 60

Ala Thr Val His Leu Pro Ala Gly Thr Thr Phe Gln Tyr Lys Tyr Ile
 65 70 75 80

Arg Lys Glu Thr Asp Gly Ser Val Thr Trp Glu Ser Asp Pro Asn Arg
 85 90 95

Ser Tyr Thr Val Pro Ser Ser Cys Gly Val Ser Ser Ala Thr Glu Ser
 100 105 110

Asp Thr Trp Arg
115

<210> 25
<211> 133
<212> PRT
<213> *Penicillium cf. miczynskii*

<220>
<221> MISC_FEATURE
<222> (1)..(133)
<223> CBM

<400> 25

Thr Thr Thr Gly Gly Thr Thr Thr Ser Gln Gly Ser Thr Thr Thr Thr
1 5 10 15

Ser Lys Thr Ser Thr Thr Thr Ser Ser Cys Thr Ala Pro Thr Ser Val
20 25 30

Ala Val Thr Phe Asp Leu Ile Ala Thr Thr Val Tyr Asp Glu Asn Val
35 40 45

Gln Leu Ala Gly Ser Ile Ser Ala Leu Gly Ser Trp Asp Thr Ser Ser
50 55 60

Ala Ile Arg Leu Ser Ala Ser Gln Tyr Thr Ser Ser Asn His Leu Trp
65 70 75 80

Tyr Val Ala Val Ser Leu Pro Ala Gly Gln Val Phe Gln Tyr Lys Tyr
85 90 95

Ile Arg Val Ala Ser Ser Gly Thr Ile Thr Trp Glu Ser Asp Pro Asn
100 105 110

Leu Ser Tyr Thr Val Pro Val Ala Cys Ala Ala Thr Ala Val Thr Ile
115 120 125

Ser Asp Thr Trp Arg
130

<210> 26
<211> 116
<212> PRT
<213> *Mz1 Penicillium sp.*

<220>

<221> MISC_FEATURE

<222> (1)..(116)

<223> CBM

<400> 26

Thr Lys Thr Ser Thr Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala
 1 5 10 15

Val Thr Phe Asp Leu Ile Ala Thr Thr Thr Tyr Gly Glu Asn Ile Lys
 20 25 30

Ile Ala Gly Ser Ile Ala Ala Leu Gly Ala Trp Asp Thr Asp Asp Ala
 35 40 45

Val Ala Leu Ser Ala Ala Asp Tyr Thr Asp Ser Asp His Leu Trp Phe
 50 55 60

Val Thr Gln Ser Ile Pro Ala Gly Thr Val Phe Glu Tyr Lys Tyr Ile
 65 70 75 80

Arg Val Glu Ser Asp Gly Thr Ile Glu Trp Glu Ser Asp Pro Asn Arg
 85 90 95

Ser Tyr Thr Val Pro Ala Ala Cys Ala Thr Thr Ala Val Thr Glu Ser
 100 105 110

Asp Thr Trp Arg
 115

<210> 27

<211> 114

<212> PRT

<213> Thysanophora sp.

<220>

<221> MISC_FEATURE

<222> (1)..(114)

<223> CBM

<400> 27

Phe Thr Ser Thr Thr Lys Thr Ser Cys Thr Thr Pro Thr Ser Val Ala
 1 5 10 15

Val Thr Phe Asp Leu Ile Ala Thr Thr Thr Tyr Gly Glu Ser Ile Arg
 20 25 30

Leu Val Gly Ser Ile Ser Glu Leu Gly Asp Trp Asp Thr Gly Ser Ala
 35 40 45

Ile Ala Leu His Ala Thr Asp Tyr Thr Asp Ser Asp His Leu Trp Phe
 50 55 60

Val Thr Val Gly Leu Pro Ala Gly Ala Ser Phe Glu Tyr Lys Tyr Ile
 65 70 75 80

Arg Val Glu Ser Ser Gly Thr Ile Glu Trp Glu Ser Asp Pro Asn Arg
 85 90 95

Ser Tyr Thr Val Pro Ala Ala Cys Ala Thr Thr Ala Val Thr Glu Ser
 100 105 110

Asp Thr

<210> 28
 <211> 111
 <212> PRT
 <213> Humicola grisea var. thermoidea

<220>
 <221> MISC_FEATURE
 <222> (1)..(111)
 <223> CBM

<400> 28

Ala Asp Ala Ser Glu Val Tyr Val Thr Phe Asn Glu Arg Val Ser Thr
 1 5 10 15

Ala Trp Gly Glu Thr Ile Lys Val Val Gly Asn Val Pro Ala Leu Gly
 20 25 30

Asn Trp Asp Thr Ser Lys Ala Val Thr Leu Ser Ala Ser Gly Tyr Lys
 35 40 45

Ser Asn Asp Pro Leu Trp Ser Ile Thr Val Pro Ile Lys Ala Thr Gly
 50 55 60

Ser Ala Val Gln Tyr Lys Tyr Ile Lys Val Gly Thr Asn Gly Lys Ile
 65 70 75 80

Thr Trp Glu Ser Asp Pro Asn Arg Ser Ile Thr Leu Gln Thr Ala Ser
 85 90 95

Ser Ala Gly Lys Cys Ala Ala Gln Thr Val Asn Asp Ser Trp Arg
 100 105 110

<210> 29
 <211> 108
 <212> PRT
 <213> Aspergillus niger

<220>
 <221> MISC_FEATURE
 <222> (1)..(108)
 <223> CBM

<400> 29

Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala Thr
 1 5 10 15

Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu
 20 25 30

Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr
 35 40 45

Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu Pro Ala Gly
 50 55 60

Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser Val
 65 70 75 80

Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys
 85 90 95

Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
 100 105

<210> 30
 <211> 97
 <212> PRT
 <213> Athelia rolfsii

<220>
 <221> MISC_FEATURE
 <222> (1)..(97)
 <223> CBM

<400> 30

Val Glu Val Thr Phe Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn
 1 5 10 15

Ile Tyr Ile Thr Gly Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala
 20 25 30

Asn Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr
 35 40 45

Ile Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile
 50 55 60

Asp Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile
 65 70 75 80

Thr Thr Pro Ala Ser Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu
 85 90 95

Ser

<210> 31
 <211> 640
 <212> PRT
 <213> Aspergillus kawachi alpha-amylase

<220>
 <221> mat_peptide
 <222> (22)..(640)
 <400> 31

Met Arg Val Ser Thr Ser Ser Ile Ala Leu Ala Val Ser Leu Phe Gly
 -20 -15 -10

Lys Leu Ala Leu Gly Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile
 -5 -1 1 5 10

Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr
 15 20 25

Ala Thr Cys Asn Thr Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln
 30 35 40

Gly Ile Ile Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala
 45 50 55

Ile Trp Ile Ser Pro Ile Thr Glu Gln Leu Pro Gln Asp Thr Ser Asp
60 65 70 75

Gly Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Tyr Val Asn
80 85 90

Ser Asn Phe Gly Thr Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu
95 100 105

His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met
110 115 120

Gly Tyr Ala Gly Asn Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro
125 130 135

Phe Asp Ser Ser Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp
140 145 150 155

Asp Asn Leu Thr Met Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val
160 165 170

Ser Leu Pro Asp Leu Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp
175 180 185

Tyr Asp Trp Val Ala Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu
190 195 200

Arg Ile Asp Ser Val Glu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr
205 210 215

Gln Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn
220 225 230 235

Pro Ala Leu Asp Cys Pro Tyr Gln Lys Tyr Leu Asp Gly Val Leu Asn
240 245 250

Tyr Pro Ile Tyr Trp Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly
255 260 265

Ser Ile Ser Asn Leu Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys
270 275 280

Ser Asp Pro Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro
285 290 295

Arg Phe Ala Ser Tyr Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu
300 305 310 315

Ser Tyr Ile Phe Leu Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu
320 325 330

Glu Gln His Tyr Ser Gly Gly Asp Val Pro Tyr Asn Arg Glu Ala Thr
335 340 345

Trp Leu Ser Gly Tyr Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala
350 355 360

Thr Thr Asn Ala Ile Arg Lys Leu Ala Ile Ser Ala Asp Ser Asp Tyr
365 370 375

Ile Thr Tyr Lys Asn Asp Pro Ile Tyr Thr Asp Ser Asn Thr Ile Ala
380 385 390 395

Met Arg Lys Gly Thr Ser Gly Ser Gln Ile Ile Thr Val Leu Ser Asn
400 405 410

Lys Gly Ser Ser Gly Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly
415 420 425

Tyr Thr Ser Gly Thr Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val
430 435 440

Thr Val Asp Ser Asn Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu
445 450 455

Pro Arg Val Leu Leu Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys
460 465 470 475

Gly Gly Ser Gly Asn Thr Thr Thr Thr Thr Thr Ala Ala Thr Ser Thr
480 485 490

Ser Lys Ala Thr Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr
495 500 505

Ser Ser Ser Cys Thr Ala Thr Ser Thr Thr Leu Pro Ile Thr Phe Glu
510 515 520

Glu Leu Val Thr Thr Thr Tyr Gly Glu Glu Val Tyr Leu Ser Gly Ser
525 530 535

Ile Ser Gln Leu Gly Glu Trp His Thr Ser Asp Ala Val Lys Leu Ser
540 545 550 555

Ala Asp Asp Tyr Thr Ser Ser Asn Pro Glu Trp Ser Val Thr Val Ser
560 565 570

Leu Pro Val Gly Thr Thr Phe Glu Tyr Lys Phe Ile Lys Val Asp Glu
575 580 585

Gly Gly Ser Val Thr Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
590 595 600

Pro Glu Cys Gly Ser Gly Ser Gly Glu Thr Val Val Asp Thr Trp Arg
605 610 615

<210> 32
<211> 1860
<212> DNA
<213> Artificial

<220>
<223> hybrid consisting of Aspergillus niger acid alpha-amylase
catalytic domain-Aspergillus kawachii alpha-amylase
linker-Aspergillus niger glucoamylase CBM

<220>
<221> CDS
<222> (1)..(1860)
<223> hybrid

<400> 32 48
ctg tcg gct gca gaa tgg cgc act cag tcg att tac ttc cta ttg acg
Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
1 5 10 15

gat cgg ttc ggt agg acg gac aat tcg acg aca gct aca tgc gat acg 96
Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
20 25 30

ggt gac caa atc tat tgt ggt ggc agt tgg caa gga atc atc aac cat 144
Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
35 40 45

ctg gat tat atc cag ggc atg gga ttc acg gcc atc tgg atc tcg cct 192
Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
50 55 60

atc act gaa cag ctg ccc cag gat act gct gat ggt gaa gct tac cat 240
Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
65 70 75 80

gga tat tgg cag cag aag ata tac gac gtg aac tcc aac ttc ggc act Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr 85 90 95	288
gca gat gac ctc aag tcc ctc tca gat gcg ctt cat gcc cgc gga atg Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met 100 105 110	336
tac ctc atg gtg gac gtc gtc cct aac cac atg ggc tac gcc ggc aac Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn 115 120 125	384
ggc aac gat gta gac tac agc gtc ttc gac ccc ttc gat tcc tcc tcc Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser 130 135 140	432
tac ttc cac cca tac tgc ctg atc aca gat tgg gac aac ttg acc atg Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met 145 150 155 160	480
gtc caa gat tgt tgg gag ggt gac acc atc gta tct ctg cca gac cta Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu 165 170 175	528
aac acc acc gaa act gcc gtg aga aca atc tgg tat gac tgg gta gcc Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala 180 185 190	576
gac ctg gta tcc aat tat tca gtc gac gga ctc cgc atc gac agt gtc Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val 195 200 205	624
ctc gaa gtc gaa cca gac ttc ttc ccg ggc tac cag gaa gca gca ggt Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly 210 215 220	672
gtc tac tgc gtc ggc gaa gtc gac aac ggc aac cct gcc ctc gac tgc Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys 225 230 235 240	720
cca tac cag aag gtc ctg gac ggc gtc ctc aac tat ccg atc tac tgg Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp 245 250 255	768
caa ctc ctc tac gcc ttc gaa tcc tcc agc ggc agc atc agc aat ctc Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu 260 265 270	816
tac aac atg atc aaa tcc gtc gca agc gac tgc tcc gat ccg aca cta Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu 275 280 285	864
ctc ggc aac ttc atc gaa aac cac gac aat ccc cgt ttc gcc tcc tac Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr 290 295 300	912
acc tcc gac tac tcg caa gcc aaa aac gtc ctc agc tac atc ttc ctc Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu 305 310 315 320	960

tcc gac ggc atc ccc atc gtc tac gcc ggc gaa gaa cag cac tac tcc Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser 325 330 335	1008
ggc ggc aag gtg ccc tac aac cgc gaa gcg acc tgg ctt tca ggc tac Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr 340 345 350	1056
gac acc tcc gca gag ctg tac acc tgg ata gcc acc acg aac gcg atc Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile 355 360 365	1104
cgc aaa cta gcc atc tca gct gac tcg gcc tac att acc tac gcg aat Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn 370 375 380	1152
gat gca ttc tac act gac agc aac acc atc gca atg cgc aaa ggc acc Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr 385 390 395 400	1200
tca ggg agc caa gtc atc acc gtc ctc tcc aac aaa ggc tcc tca gga Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly 405 410 415	1248
agc agc tac acc ctg acc ctc agc gga agc ggc tac aca tcc ggc acg Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr 420 425 430	1296
aag ctg atc gaa gcg tac aca tgc aca tcc gtg acc gtg gac tcg agc Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser 435 440 445	1344
ggc gat att ccc gtg ccg atg gcg tcg gga tta ccg aga gtt ctt ctg Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu 450 455 460	1392
ccc gcg tcc gtc gtc gat agc tct tcg ctc tgt ggc ggg agc gga aga Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg 465 470 475 480	1440
aca acc acg acc aca act gct gct gct act agt aca tcc aaa gcc acc Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr 485 490 495	1488
acc tcc tct tct tct tct tct gct gct gct act act tct tca tca tgt Thr Ser Ser Ser Ser Ser Ser Ala Ala Thr Thr Ser Ser Ser Cys 500 505 510	1536
acc act ccc acc gcc gtg gct gtg act ttc gat ctg aca gct acc acc Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala Thr Thr 515 520 525	1584
acc tac ggc gag aac atc tac ctg gtc gga tcg atc tct cag ctg ggt Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu Gly 530 535 540	1632
gac tgg gaa acc agc gac ggc ata gct ctg agt gct gac aag tac act Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr Thr 545 550 555 560	1680

tcc agc gac ccg ctc tgg tat gtc act gtg act ctg ccg gct ggt gag 1728
 Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu Pro Ala Gly Glu
 565 570 575

tcg ttt gag tac aag ttt atc cgc att gag agc gat gac tcc gtg gag 1776
 Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser Val Glu
 580 585 590

tgg gag agt gat ccc aac cga gaa tac acc gtt cct cag gcg tgc gga 1824
 Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys Gly
 595 600 605

acg tcg acc gcg acg gtg act gac acc tgg cgg tag 1860
 Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
 610 615

<210> 33
 <211> 619
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 33

Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
 1 5 10 15

Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
 20 25 30

Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
 35 40 45

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
 50 55 60

Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
 65 70 75 80

Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
 85 90 95

Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
 100 105 110

Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn
 115 120 125

Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
 130 135 140

Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
 145 150 155 160

Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
 165 170 175

Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala
 180 185 190

Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
 195 200 205

Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly
 210 215 220

Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys
 225 230 235 240

Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
 245 250 255

Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu
 260 265 270

Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
 275 280 285

Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
 290 295 300

Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu
 305 310 315 320

Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser
 325 330 335

Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
 340 345 350

Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile
 355 360 365

Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn
 370 375 380

Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr
 385 390 395 400

Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
 405 410 415

Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
 420 425 430

Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
 435 440 445

Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu
 450 455 460

Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg
 465 470 475 480

Thr Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr
 485 490 495

Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser Cys
 500 505 510

Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala Thr Thr
 515 520 525

Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu Gly
 530 535 540

Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr Thr
 545 550 555 560

Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu Pro Ala Gly Glu
 565 570 575

Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser Val Glu
 580 585 590

Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys Gly
 595 600 605

Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
610 615

<210> 34
<211> 1827
<212> DNA
<213> Artificial

<220>
<223> Hybrid containing Aspergillus niger acid alpha-amylase catalytic domain-Aspergillus kawachii alpha-amylase linker-Athelia rolfsii glucoamylase CBD

<220>
<221> CDS
<222> (1)..(1827)
<223> Hybrid

<400> 34
ctg tcg gct gca gaa tgg cgc act cag tcg att tac ttc cta ttg acg 48
Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
1 5 10 15
gat cgg ttc ggt agg acg gac aat tcg acg aca gct aca tgc gat acg 96
Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
20 25 30
ggt gac caa atc tat tgt ggt ggc agt tgg caa gga atc atc aac cat 144
Gly Asp Gln Ile Tyr Cys Gly Tyr Ser Trp Gln Gly Ile Ile Asn His
35 40 45
ctg gat tat atc cag ggc atg gga ttc acg gcc atc tgg atc tcg cct 192
Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
50 55 60
atc act gaa cag ctg ccc cag gat act gct gat ggt gaa gct tac cat 240
Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
65 70 75 80
gga tat tgg cag cag aag ata tac gac gtg aac tcc aac ttc ggc act 288
Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
85 90 95
gca gat gac ctc aag tcc ctc tca gat gcg ctt cat gcc cgc gga atg 336
Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
100 105 110
tac ctc atg gtg gac gtc gtc cct aac cac atg ggc tac gcc ggc aac 384
Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn
115 120 125
ggc aac gat gta gac tac agc gtc ttc gac ccc ttc gat tcc tcc tcc 432
Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
130 135 140
tac ttc cac cca tac tgc ctg atc aca gat tgg gac aac ttg acc atg 480
Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
145 150 155 160

gtc caa gat tgt tgg gag ggt gac acc atc gta tct ctg cca gac cta Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu 165 170 175	528
aac acc acc gaa act gcc gtg aga aca atc tgg tat gac tgg gta gcc Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala 180 185 190	576
gac ctg gta tcc aat tat tca gtc gac gga ctc cgc atc gac agt gtc Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val 195 200 205	624
ctc gaa gtc gaa cca gac ttc ttc ccg ggc tac cag gaa gca gca ggt Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly 210 215 220	672
gtc tac tgc gtc ggc gaa gtc gac aac ggc aac cct gcc ctc gac tgc Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys 225 230 235 240	720
cca tac cag aag gtc ctg gac ggc gtc ctc aac tat ccg atc tac tgg Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp 245 250 255	768
caa ctc ctc tac gcc ttc gaa tcc tcc agc ggc agc atc agc aat ctc Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu 260 265 270	816
tac aac atg atc aaa tcc gtc gca agc gac tgc tcc gat ccg aca cta Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu 275 280 285	864
ctc ggc aac ttc atc gaa aac cac gac aat ccc cgt ttc gcc tcc tac Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr 290 295 300	912
acc tcc gac tac tgc caa gcc aaa aac gtc ctc agc tac atc ttc ctc Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu 305 310 315 320	960
tcc gac ggc atc ccc atc gtc tac gcc ggc gaa gaa cag cac tac tcc Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser 325 330 335	1008
ggc ggc aag gtg ccc tac aac cgc gaa ggc acc tgg ctt tca ggc tac Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr 340 345 350	1056
gac acc tcc gca gag ctg tac acc tgg ata gcc acc acg aac ggc atc Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile 355 360 365	1104
cgc aaa cta gcc atc tca gct gac tgc gcc tac att acc tac ggc aat Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn 370 375 380	1152
gat gca ttc tac act gac agc aac acc atc gca atg cgc aaa ggc acc Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr 385 390 395 400	1200

tca ggg agc caa gtc atc acc gtc ctc tcc aac aaa ggc tcc tca gga Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly 405 410 415	1248
agc agc tac acc ctg acc ctc agc gga agc ggc tac aca tcc ggc acg Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr 420 425 430	1296
aag ctg atc gaa gcg tac aca tgc aca tcc gtg acc gtg gac tcg agc Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser 435 440 445	1344
ggc gat att ccc gtg ccg atg gcg tcg gga tta ccg aga gtt ctt ctg Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu 450 455 460	1392
ccc gcg tcc gtc gtc gat agc tct tcg ctc tgt ggc ggg agc gga aga Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg 465 470 475 480	1440
aca acc acg acc aca act gct gct gct act agt aca tcc aaa gcc acc Thr Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr 485 490 495	1488
acc tcc tct tct tct tct tct gct gct gct act act tct tca tca gtc Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser Val 500 505 510	1536
gag gtc act ttc gac gtt tac gct acc aca gta tat ggc cag aac atc Glu Val Thr Phe Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile 515 520 525	1584
tat atc acc ggt gat gtg agt gag ctc ggc aac tgg aca ccc gcc aat Tyr Ile Thr Gly Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn 530 535 540	1632
ggt gtt gca ctc tct tct gct aac tac ccc acc tgg agt gcc acg atc Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile 545 550 555 560	1680
gct ctc ccc gct gac acg aca atc cag tac aag tat gtc aac att gac Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp 565 570 575	1728
ggc agc acc gtc atc tgg gag gat gct atc agc aat cgc gag atc acg Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr 580 585 590	1776
acg ccc gcc agc ggc aca tac acc gaa aaa gac act tgg gat gaa tct Thr Pro Ala Ser Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser 595 600 605	1824
tag	1827

<210> 35
 <211> 608
 <212> PRT
 <213> Artificial

<220>

<223> Synthetic Construct

<400> 35

Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
 1 5 10 15

Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
 20 25 30

Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
 35 40 45

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
 50 55 60

Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
 65 70 75 80

Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
 85 90 95

Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
 100 105 110

Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn
 115 120 125

Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
 130 135 140

Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
 145 150 155 160

Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
 165 170 175

Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala
 180 185 190

Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
 195 200 205

Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly
 210 215 220

Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys
 225 230 235 240

Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
 245 250 255

Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu
 260 265 270

Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
 275 280 285

Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
 290 295 300

Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu
 305 310 315 320

Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser
 325 330 335

Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
 340 345 350

Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile
 355 360 365

Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn
 370 375 380

Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr
 385 390 395 400

Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
 405 410 415

Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
 420 425 430

Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
 435 440 445

Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu
 450 455 460

Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg
465 470 475 480

Thr Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr
485 490 495

Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser Val
500 505 510

Glu Val Thr Phe Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile
515 520 525

Tyr Ile Thr Gly Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn
530 535 540

Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile
545 550 555 560

Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp
565 570 575

Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr
580 585 590

Thr Pro Ala Ser Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
595 600 605

<210> 36
<211> 1863
<212> DNA
<213> Artificial

<220>
<223> Hybrid consisting of A.oryzae alpha-amylase catalytic domain-A.
kawachii alpha-amylase linker-A. kawachi alpha-amylase CBD

<220>
<221> CDS
<222> (1)..(1863)
<223> Hybrid

<400> 36
gca acg cct gcg gac tgg cga tcg caa tcc att tat ttc ctt ctc acg
Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1 5 10 15

48

gat cga ttt gca agg acg gat ggg tcg acg act gcg act tgt aat act Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr 20 25 30	96
gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc atc atc gac aag Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys 35 40 45	144
ttg gac tat atc cag gga atg ggc ttc aca gcc atc tgg atc acc ccc Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro 50 55 60	192
gtt aca gcc cag ctg ccc cag acc acc gca tat gga gat gcc tac cat Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His 65 70 75 80	240
ggc tac tgg cag cag gat ata tac tct ctg aac gaa aac tac ggc act Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr 85 90 95	288
gca gat gac ttg aag gcg ctc tct tcg gcc ctt cat gag agg ggg atg Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met 100 105 110	336
tat ctt atg gtc gat gtg gtt gct aac cat atg ggc tat gat gga gcg Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala 115 120 125	384
ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc agt tcc caa gac Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp 130 135 140	432
tac ttc cac ccg ttc tgt ttc att caa aac tat gaa gat cag act cag Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln 145 150 155 160	480
gtt gag gat tgc tgg cta gga gat aac act gtc tcc ttg cct gat ctc Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu 165 170 175	528
gat acc acc aag gat gtg gtc aag aat gaa tgg tac gac tgg gtg gga Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly 180 185 190	576
tca ttg gta tcg aac tac tcc att gac ggc ctc cgt atc gac aca gta Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val 195 200 205	624
aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac aaa gcc gca ggc Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly 210 215 220	672
gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg gcc tac act tgt Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys 225 230 235 240	720
ccc tac cag aac gtc atg gac ggc gta ctg aac tat ccc att tac tat Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr 245 250 255	768

cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc atg gac gac ctc Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu 260 265 270	816
tac aac atg atc aac acc gtc aaa tcc gac tgt cca gac tca aca ctc Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu 275 280 285	864
ctg ggc aca ttc gtc gag aac cac gac aac cca cgg ttc gct tct tac Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr 290 295 300	912
acc aac gac ata gcc ctc gcc aag aac gtc gca gca ttc atc atc ctc Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu 305 310 315 320	960
aac gac gga atc ccc atc atc tac gcc ggc caa gaa cag cac tac gcc Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala 325 330 335	1008
ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg ctc tcg ggc tac Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr 340 345 350	1056
ccg acc gac agc gag ctg tac aag tta att gcc tcc gcg aac gca atc Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala Asn Ala Ile 355 360 365	1104
cgg aac tat gcc att agc aaa gat aca gga ttc gtg acc tac aag aac Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn 370 375 380	1152
tgg ccc atc tac aaa gac gac aca acg atc gcc atg cgc aag ggc aca Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr 385 390 395 400	1200
gat ggg tcg cag atc gtg act atc ttg tcc aac aag ggt gct tcg ggt Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly 405 410 415	1248
gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac aca gcc ggc cag Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln 420 425 430	1296
caa ttg acg gag gtc att ggc tgc acg acc gtg acg gtt ggt tcg gat Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp 435 440 445	1344
gga aat gtg cct gtt cct atg gca ggt ggg cta cct agg gta ttg tat Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr 450 455 460	1392
ccg act gag aag ttg gca ggt agc aag atc tgt agt agc tcg gga aga Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser Gly Arg 465 470 475 480	1440
aca acc acg acc aca act gct gct gct act agt aca tcc aaa gcc acc Thr Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr 485 490 495	1488

acc tcc tct tct tct tct tct gct gct gct act act tct tca tca tgc 1536
 Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser Cys
 500 505 510
 acc gca aca agc acc acc ctc ccc atc acc ttc gaa gaa ctc gtc acc 1584
 Thr Ala Thr Ser Thr Thr Leu Pro Ile Thr Phe Glu Glu Leu Val Thr
 515 520 525
 act acc tac ggg gaa gaa gtc tac ctc agc gga tct atc tcc cag ctc 1632
 Thr Thr Tyr Gly Glu Glu Val Tyr Leu Ser Gly Ser Ile Ser Gln Leu
 530 535 540
 gga gag tgg gat acg agt gac gcg gtg aag ttg tcc gcg gat gat tat 1680
 Gly Glu Trp Asp Thr Ser Asp Ala Val Lys Leu Ser Ala Asp Asp Tyr
 545 550 555 560
 acc tcg agt aac ccc gag tgg tct gtt act gtg tcg ttg ccg gtg ggg 1728
 Thr Ser Ser Asn Pro Glu Trp Ser Val Thr Val Ser Leu Pro Val Gly
 565 570 575
 acg acc ttc gag tat aag ttt att aag gtc gat gag ggt gga agt gtg 1776
 Thr Thr Phe Glu Tyr Lys Phe Ile Lys Val Asp Glu Gly Gly Ser Val
 580 585 590
 act tgg gaa agt gat ccg aat agg gag tat act gtg cct gaa tgt ggg 1824
 Thr Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Glu Cys Gly
 595 600 605
 aat ggg agt ggg gag acg gtg gtt gat acg tgg agg tag 1863
 Asn Gly Ser Gly Glu Thr Val Val Asp Thr Trp Arg
 610 615 620

<210> 37
 <211> 620
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 37

Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
 1 5 10 15

Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr
 20 25 30

Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
 35 40 45

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
 50 55 60

Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His
65 70 75 80

Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
85 90 95

Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
100 105 110

Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
115 120 125

Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
130 135 140

Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln
145 150 155 160

Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
165 170 175

Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
180 185 190

Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
195 200 205

Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
210 215 220

Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys
225 230 235 240

Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
245 250 255

Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu
260 265 270

Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
275 280 285

Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
290 295 300

Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
 305 310 315 320

Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
 325 330 335

Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
 340 345 350

Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala Asn Ala Ile
 355 360 365

Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn
 370 375 380

Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr
 385 390 395 400

Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
 405 410 415

Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln
 420 425 430

Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp
 435 440 445

Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
 450 455 460

Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser Gly Arg
 465 470 475 480

Thr Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr
 485 490 495

Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser Cys
 500 505 510

Thr Ala Thr Ser Thr Thr Leu Pro Ile Thr Phe Glu Glu Leu Val Thr
 515 520 525

Thr Thr Tyr Gly Glu Glu Val Tyr Leu Ser Gly Ser Ile Ser Gln Leu
 530 535 540

Gly Glu Trp Asp Thr Ser Asp Ala Val Lys Leu Ser Ala Asp Asp Tyr
 545 550 555 560

Thr Ser Ser Asn Pro Glu Trp Ser Val Thr Val Ser Leu Pro Val Gly
 565 570 575

Thr Thr Phe Glu Tyr Lys Phe Ile Lys Val Asp Glu Gly Gly Ser Val
 580 585 590

Thr Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Glu Cys Gly
 595 600 605

Asn Gly Ser Gly Glu Thr Val Val Asp Thr Trp Arg
 610 615 620

<210> 38
 <211> 1767
 <212> DNA
 <213> Artificial

<220>
 <223> Hybrid consisting of A. niger acid alpha-amylase catalytic
 domain- A.rolfsii glucoamylase linker- A. rolfsii glucoamylase
 CBM

<220>
 <221> CDS
 <222> (1)..(1767)
 <223> Hybrid

<400> 38
 ctg tcg gct gca gaa tgg cgc act cag tcg att tac ttc cta ttg acg 48
 Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
 1 5 10 15

gat cgg ttc ggt agg acg gac aat tcg acg aca gct aca tgc gat acg 96
 Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
 20 25 30

ggt gac caa atc tat tgt ggt ggc agt tgg caa gga atc atc aac cat 144
 Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
 35 40 45

ctg gat tat atc cag ggc atg gga ttc acg gcc atc tgg atc tcg cct 192
 Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
 50 55 60

atc act gaa cag ctg ccc cag gat act gct gat ggt gaa gct tac cat 240
 Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
 65 70 75 80

gga tat tgg cag cag aag ata tac gac gtg aac tcc aac ttc ggc act Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr 85 90 95	288
gca gat gac ctc aag tcc ctc tca gat gcg ctt cat gcc cgc gga atg Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met 100 105 110	336
tac ctc atg gtg gac gtc gtc cct aac cac atg ggc tac gcc ggc aac Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn 115 120 125	384
ggc aac gat gta gac tac agc gtc ttc gac ccc ttc gat tcc tcc tcc Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser 130 135 140	432
tac ttc cac cca tac tgc ctg atc aca gat tgg gac aac ttg acc atg Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met 145 150 155 160	480
gtc caa gat tgt tgg gag ggt gac acc atc gta tct ctg cca gac cta Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu 165 170 175	528
aac acc acc gaa act gcc gtg aga aca atc tgg tat gac tgg gta gcc Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala 180 185 190	576
gac ctg gta tcc aat tat tca gtc gac gga ctc cgc atc gac agt gtc Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val 195 200 205	624
ctc gaa gtc gaa cca gac ttc ttc ccg ggc tac cag gaa gca gca ggt Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly 210 215 220	672
gtc tac tgc gtc ggc gaa gtc gac aac ggc aac cct gcc ctc gac tgc Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys 225 230 235 240	720
cca tac cag aag gtc ctg gac ggc gtc ctc aac tat ccg atc tac tgg Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp 245 250 255	768
caa ctc ctc tac gcc ttc gaa tcc tcc agc ggc agc atc agc aat ctc Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu 260 265 270	816
tac aac atg atc aaa tcc gtc gca agc gac tgc tcc gat ccg aca cta Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu 275 280 285	864
ctc ggc aac ttc atc gaa aac cac gac aat ccc cgt ttc gcc tcc tac Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr 290 295 300	912
acc tcc gac tac tcg caa gcc aaa aac gtc ctc agc tac atc ttc ctc Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu 305 310 315 320	960

tcc gac ggc atc ccc atc gtc tac gcc ggc gaa gaa cag cac tac tcc Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser 325 330 335	1008
ggc ggc aag gtg ccc tac aac cgc gaa gcg acc tgg ctt tca ggc tac Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr 340 345 350	1056
gac acc tcc gca gag ctg tac acc tgg ata gcc acc acg aac gcg atc Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile 355 360 365	1104
cgc aaa cta gcc atc tca gct gac tcg gcc tac att acc tac gcg aat Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn 370 375 380	1152
gat gca ttc tac act gac agc aac acc atc gca atg cgc aaa ggc acc Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr 385 390 395 400	1200
tca ggg agc caa gtc atc acc gtc ctc tcc aac aaa ggc tcc tca gga Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly 405 410 415	1248
agc agc tac acc ctg acc ctc agc gga agc ggc tac aca tcc ggc acg Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr 420 425 430	1296
aag ctg atc gaa gcg tac aca tgc aca tcc gtg acc gtg gac tcg agc Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser 435 440 445	1344
ggc gat att ccc gtg ccg atg gcg tcg gga tta ccg aga gtt ctt ctg Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu 450 455 460	1392
ccc gcg tcc gtc gtc gat agc tct tcg ctc tgt ggc ggg agc gga aga Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg 465 470 475 480	1440
ggt gct aca agc ccg ggt ggc tcc tcg ggt agt gtc gag gtc act ttc Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe 485 490 495	1488
gac gtt tac gct acc aca gta tat ggc cag aac atc tat atc acc ggt Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly 500 505 510	1536
gat gtg agt gag ctc ggc aac tgg aca ccc gcc aat ggt gtt gca ctc Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu 515 520 525	1584
tct tct gct aac tac ccc acc tgg agt gcc acg atc gct ctc ccc gct Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala 530 535 540	1632

gac acg aca atc cag tac aag tat gtc aac att gac ggc agc acc gtc 1680
 Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val
 545 550 555 560

atc tgg gag gat gct atc agc aat cgc gag atc acg acg ccc gcc agc 1728
 Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser
 565 570 575

ggc aca tac acc gaa aaa gac act tgg gat gaa tct tag 1767
 Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
 580 585

<210> 39
 <211> 588
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 39

Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
 1 5 10 15

Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
 20 25 30

Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
 35 40 45

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
 50 55 60

Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
 65 70 75 80

Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
 85 90 95

Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
 100 105 110

Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn
 115 120 125

Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
 130 135 140

Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
 145 150 155 160

Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
 165 170 175

Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala
 180 185 190

Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
 195 200 205

Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly
 210 215 220

Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys
 225 230 235 240

Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
 245 250 255

Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu
 260 265 270

Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
 275 280 285

Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
 290 295 300

Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu
 305 310 315 320

Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser
 325 330 335

Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
 340 345 350

Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile
 355 360 365

Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn
 370 375 380

Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr
 385 390 395 400

Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
 405 410 415

Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
 420 425 430

Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
 435 440 445

Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu
 450 455 460

Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg
 465 470 475 480

Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe
 485 490 495

Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly
 500 505 510

Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu
 515 520 525

Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala
 530 535 540

Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val
 545 550 555 560

Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser
 565 570 575

Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
 580 585

<210> 40
 <211> 1767
 <212> DNA
 <213> Artificial

<220>
 <223> Hybrid containing A. oryzae alpha-amylase catalytic domain- A.
 rolfsii glucoamylase linker- A. rolfsii glucoamylase CBM

<220>

<221> CDS

<222> (1)..(1767)

<223> Hybrid

<400> 40

gca acg cct gcg gac tgg cga tcg caa tcc att tat ttc ctt ctc acg 48
 Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
 1 5 10 15

gat cga ttt gca agg acg gat ggg tcg acg act gcg act tgt aat act 96
 Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr
 20 25 30

gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc atc atc gac aag 144
 Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
 35 40 45

ttg gac tat atc cag gga atg ggc ttc aca gcc atc tgg atc acc ccc 192
 Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
 50 55 60

gtt aca gcc cag ctg ccc cag acc acc gca tat gga gat gcc tac cat 240
 Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His
 65 70 75 80

ggc tac tgg cag cag gat ata tac tct ctg aac gaa aac tac ggc act 288
 Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
 85 90 95

gca gat gac ttg aag gcg ctc tct tcg gcc ctt cat gag agg ggg atg 336
 Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
 100 105 110

tat ctt atg gtc gat gtg gtt gct aac cat atg ggc tat gat gga gcg 384
 Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
 115 120 125

ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc agt tcc caa gac 432
 Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
 130 135 140

tac ttc cac ccg ttc tgt ttc att caa aac tat gaa gat cag act cag 480
 Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln
 145 150 155 160

gtt gag gat tgc tgg cta gga gat aac act gtc tcc ttg cct gat ctc 528
 Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
 165 170 175

gat acc acc aag gat gtg gtc aag aat gaa tgg tac gac tgg gtg gga 576
 Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
 180 185 190

tca ttg gta tcg aac tac tcc att gac ggc ctc cgt atc gac aca gta 624
 Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
 195 200 205

aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac aaa gcc gca ggc Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly 210 215 220	672
gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg gcc tac act tgt Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys 225 230 235 240	720
ccc tac cag aac gtc atg gac ggc gta ctg aac tat ccc att tac tat Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr 245 250 255	768
cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc atg gac gac ctc Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu 260 265 270	816
tac aac atg atc aac acc gtc aaa tcc gac tgt cca gac tca aca ctc Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu 275 280 285	864
ctg ggc aca ttc gtc gag aac cac gac aac cca cgg ttc gct tct tac Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr 290 295 300	912
acc aac gac ata gcc ctc gcc aag aac gtc gca gca ttc atc atc ctc Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu 305 310 315 320	960
aac gac gga atc ccc atc atc tac gcc ggc caa gaa cag cac tac gcc Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala 325 330 335	1008
ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg ctc tcg ggc tac Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr 340 345 350	1056
ccg acc gac agc gag ctg tac aag tta att gcc tcc gcg aac gca atc Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala Asn Ala Ile 355 360 365	1104
cgg aac tat gcc att agc aaa gat aca gga ttc gtg acc tac aag aac Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn 370 375 380	1152
tgg ccc atc tac aaa gac gac aca acg atc gcc atg cgc aag ggc aca Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr 385 390 395 400	1200
gat ggg tcg cag atc gtg act atc ttg tcc aac aag ggt gct tcg ggt Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly 405 410 415	1248
gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac aca gcc ggc cag Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln 420 425 430	1296
caa ttg acg gag gtc att ggc tgc acg acc gtg acg gtt ggt tcg gat Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp 435 440 445	1344

gga aat gtg cct gtt cct atg gca ggt ggg cta cct agg gta ttg tat 1392
 Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
 450 455 460

ccg act gag aag ttg gca ggt agc aag atc tgt agt agc tcg gga aga 1440
 Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser Gly Arg
 465 470 475 480

ggt gct aca agc ccg ggt ggc tcc tcg ggt agt gtc gag gtc act ttc 1488
 Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe
 485 490 495

gac gtt tac gct acc aca gta tat ggc cag aac atc tat atc acc ggt 1536
 Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly
 500 505 510

gat gtg agt gag ctc ggc aac tgg aca ccc gcc aat ggt gtt gca ctc 1584
 Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu
 515 520 525

tct tct gct aac tac ccc acc tgg agt gcc acg atc gct ctc ccc gct 1632
 Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala
 530 535 540

gac acg aca atc cag tac aag tat gtc aac att gac ggc agc acc gtc 1680
 Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val
 545 550 555 560

atc tgg gag gat gct atc agc aat cgc gag atc acg acg ccc gcc agc 1728
 Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser
 565 570 575

ggc aca tac acc gaa aaa gac act tgg gat gaa tct tag 1767
 Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
 580 585

<210> 41
 <211> 588
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 41

Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
 1 5 10 15

Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr
 20 25 30

Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
 35 40 45

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
50 55 60

Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His
65 70 75 80

Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
85 90 95

Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
100 105 110

Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
115 120 125

Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
130 135 140

Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln
145 150 155 160

Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
165 170 175

Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
180 185 190

Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
195 200 205

Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
210 215 220

Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys
225 230 235 240

Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
245 250 255

Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu
260 265 270

Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
275 280 285

Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
 290 295 300

Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
 305 310 315 320

Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
 325 330 335

Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
 340 345 350

Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala Asn Ala Ile
 355 360 365

Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn
 370 375 380

Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr
 385 390 395 400

Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
 405 410 415

Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln
 420 425 430

Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp
 435 440 445

Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
 450 455 460

Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser Gly Arg
 465 470 475 480

Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe
 485 490 495

Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly
 500 505 510

Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu
 515 520 525

Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala
530 535 540

Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val
545 550 555 560

Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser
565 570 575

Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
580 585